

10/646950 SEQ ID NO:6

GenCore version 5.1.9

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OM nucleic - protein search, using frame_plus_n2p model

Run on: July 11, 2006, 17:21:18 ; Search time 30.5853 Seconds
 (without alignments)
 3284.476 Million cell updates/sec

Title: US-10-646-950-6
 Perfect score: 645
 Sequence: 1 cattattagccagatgaatt.....gagagacttcaagctttgaa 362

Scoring table: BLOSUM62
 Xgapop 10.0 , Xgapext 0.5
 Ygapop 10.0 , Ygapext 0.5
 Fgapop 6.0 , Fgapext 7.0
 Delop 6.0 , Delext 7.0

Searched: 2849598 seqs, 925015592 residues

Total number of hits satisfying chosen parameters: 5699196

Minimum DB seq length: 0
 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
 Maximum Match 100%
 Listing first 45 summaries

Command line parameters:

-MODEL=frame+ n2p.model -DEV=xlp
 -Q=/abss/ABSSWEB_spool/US10646950/runat_11072006_111734_6250/app_query.fasta_1
 -DB=UniProt -QFMT=fastan -SUFFIX=n2p.rup -MINMATCH=0.1 -LOOPCL=0 -LOOPEXT=0
 -UNITS=bits -START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi -LIST=45
 -DOALIGN=200 -THR_SCORE=pct -THR_MAX=100 -THR_MIN=0 -ALIGN=15 -MODE=LOCAL
 -OUTFMT=pto -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000 -HOST=abss02p
 -USER=US10646950_CGN_1_1_762_@runat_11072006_111734_6250 -NCPU=6 -ICPU=3
 -NO_MMAP -NEG_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG -DEV_TIMEOUT=120
 -WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6 -FGAPEXT=7
 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : UniProt_7.2:*
 1: uniprot_sprot:*
 2: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a
 score greater than or equal to the score of the result being printed,
 and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	567	87.9	475	1	FACE1_HUMAN	Q75844 homo sapien
2	558	86.5	475	1	FACE1_MOUSE	Q80w54 mus musculu
3	554	85.9	493	2	Q5R6Y6_PONPY	Q5r6y6 pongo pygma
4	533	82.6	465	2	Q640V5_XENLA	Q640v5 xenopus lae
5	510	79.1	468	2	Q802Z1_BRARE	Q802z1 brachydanio
6	509	78.9	485	2	Q4RMB6_TETNG	Q4rmb6 tetraodon n
7	317.5	49.2	126	2	Q5BXX4_SCHJA	Q5bxx4 schistosoma
8	304.5	47.2	472	2	Q3Y6B8_TAESO	Q3y6b8 taenia soli
9	296.5	46.0	451	2	Q9V7W7_DROME	Q9v7w7 drosophila
10	271.5	42.1	394	2	Q5TSY1_ANOGA	Q5tsy1 anopheles g
11	271.5	42.1	453	2	Q7QA21_ANOGA	Q7qa21 anopheles g
12	243	37.7	425	2	Q6EPN8_ORYSA	Q6epn8 oryza sativ
13	242.5	37.6	456	2	Q2UGJ7_ASPOR	Q2ugj7 aspergillus
14	240.5	37.3	460	2	Q55UG3_CRYNE	Q55ug3 cryptococcu
15	240.5	37.3	460	2	Q5KHY1_CRYNE	Q5khy1 cryptococcu

16	237	36.7	424	2	Q8RX88_ARATH	Q8rx88	arabidopsis
17	237	36.7	424	2	Q93ZV9_ARATH	Q93zv9	arabidopsis
18	236.5	36.7	479	2	Q4WP06_ASPFU	Q4wp06	aspergillus
19	234.5	36.4	456	2	Q7SI78_EMENI	Q7si78	emericella
20	233	36.1	424	2	Q94FS8_ARATH	Q94fs8	arabidopsis
21	231.5	35.9	442	2	Q7RVV7_NEUCR	Q7rvv7	neurospora
22	231.5	35.9	446	2	Q6BMD9_DEBHA	Q6bmd9	debaryomyce
23	231.5	35.9	462	2	Q9C2C0_NEUCR	Q9c2c0	neurospora
24	229.5	35.6	867	2	Q4IA57_GIBZE	Q4ia57	gibberella
25	223.5	34.7	456	2	Q59UR6_CANAL	Q59ur6	candida alb
26	223.5	34.7	456	2	Q8IHA2_DROME	Q8iha2	drosophila
27	220.5	34.2	447	2	Q9V7W6_DROME	Q9v7w6	drosophila
28	217.5	33.7	453	2	Q56D07_PARBR	Q56d07	paracoccidi
29	213	33.0	459	2	Q9M139_ARATH	Q9m139	arabidopsis
30	211.5	32.8	442	2	Q61XW2_CAEER	Q61xw2	caenorhabdi
31	204.5	31.7	442	2	Q9XVE5_CAEEL	Q9xve5	caenorhabdi
32	190.5	29.5	453	1	STE24_YEAST	P47154	saccharomyc
33	189.5	29.4	474	1	STE24_SCHPO	Q10071	schizosacch
34	185	28.7	419	2	Q967X5_PHYPO	Q967x5	physarum po
35	176.5	27.4	456	2	Q6CR94_KLULA	Q6cr94	kluyveromyc
36	174	27.0	426	2	Q54FH7_DICDI	Q54fh7	dictyosteli
37	173.5	26.9	456	2	Q9V7W5_DROME	Q9v7w5	drosophila
38	169.5	26.3	444	2	Q4N3R0_THEPA	Q4n3r0	theileria p
39	167.5	26.0	438	2	Q4UFQ9_THEAN	Q4ufq9	theileria a
40	166.5	25.8	316	2	O04602_ARATH	O04602	arabidopsis
41	161.5	25.0	460	2	Q6FQ89_CANGA	Q6fq89	candida gla
42	156.5	24.3	422	2	Q3AS21_CHLCH	Q3as21	chlorobium
43	156.5	24.3	427	2	Q38E89_9TRYP	Q38e89	trypanosoma
44	156.5	24.3	453	2	Q2LYG7_9DELT	Q2lyg7	syntrophus
45	153	23.7	410	2	Q3XRV0_9PROT	Q3xrv0	magnetococc

ALIGNMENTS

RESULT 1

FACE1_HUMAN

ID FACE1_HUMAN STANDARD; PRT; 475 AA.
AC O75844; Q8NDZ8; Q9UBQ2;
DT 15-JUL-1999, integrated into UniProtKB/Swiss-Prot.
DT 27-APR-2001, sequence version 2.
DT 07-FEB-2006, entry version 50.
DE CAAX prenyl protease 1 homolog (EC 3.4.24.84) (Prenyl protein-specific
DE endoprotease 1) (Farnesylated proteins-converting enzyme 1) (FACE-1)
DE (Zinc metalloproteinase Ste24 homolog).
GN Name=ZMPSTE24; Synonyms=FACE1, STE24;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE [MRNA].
RC TISSUE=Brain;
RX MEDLINE=99177429; PubMed=10076063; DOI=10.1016/S0304-4165(98)00170-6;
RA Kumagai H., Kawamura Y., Yanagisawa K., Komano H.;
RT "Identification of a human cDNA encoding a novel protein structurally
RT related to the yeast membrane-associated metalloprotease, Ste24p.";
RL Biochim. Biophys. Acta 1426:468-474(1999).
RN [2]
RP NUCLEOTIDE SEQUENCE [MRNA].
RC TISSUE=B-cell, and Fetal brain;
RX MEDLINE=98365461; PubMed=9700155; DOI=10.1083/jcb.142.3.635;
RA Tam A., Nouvet F.J., Fujimura-Kamada K., Slunt H., Sisodia S.S.,
RA Michaelis S.;
RT "Dual roles for Ste24p in yeast a-factor maturation: NH2-terminal
RT proteolysis and COOH-terminal CAAX processing.";
RL J. Cell Biol. 142:635-649(1998).
RN [3]
RP NUCLEOTIDE SEQUENCE [MRNA].
RC TISSUE=Ovary;
RX MEDLINE=99303558; PubMed=10373325; DOI=10.1006/geno.1999.5834;

RA Freije J.M.P., Blay P., Pendas A.M., Cadinanos J., Crespo P.,
 RA Lopez-Otin C.;
 RT "Identification and chromosomal location of two human genes encoding
 RT enzymes potentially involved in proteolytic maturation of farnesylated
 RT proteins.";
 RL Genomics 58:270-280(1999).
 RN [4]
 RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
 RG Human chromosome 1 international sequencing consortium;
 RL Submitted (FEB-2000) to the EMBL/GenBank/DBJ databases.
 RN [5]
 RP NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA].
 RC TISSUE=Testis;
 RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.J., Ustin T.B., Toshiyuki S., Carninci P., Prange C.,
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
 RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahey J., Helton E., Kettelman M., Madan A., Rodrigues S., Sanchez A.,
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
 RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
 RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
 RT "Generation and initial analysis of more than 15,000 full-length human
 RT and mouse cDNA sequences.";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 RN [6]
 RP VARIANT MADB ARG-340.
 RX MEDLINE=22793839; PubMed=12913070; DOI=10.1093/hmg/ddg213;
 RA Agarwal A.K., Fryns J.-P., Auchus R.J., Garg A.;
 RT "Zinc metalloproteinase, ZMPSTE24, is mutated in mandibuloacral
 RT dysplasia.";
 RL Hum. Mol. Genet. 12:1995-2001(2003).
 CC -!- FUNCTION: Proteolytically removes the C-terminal three residues of
 CC farnesylated proteins. Acts on lamin A/C.
 CC -!- CATALYTIC ACTIVITY: The peptide bond hydrolyzed can be designated
 CC -C[-A-A-X in which C is an S-isoprenylated cysteine residue, A is
 CC usually aliphatic and X is the C-terminal residue of the substrate
 CC protein, and may be any of several amino acids.
 CC -!- COFACTOR: Binds 1 zinc ion per subunit (By similarity).
 CC -!- SUBCELLULAR LOCATION: Integral membrane protein. Endoplasmic
 CC reticulum and possibly also the Golgi compartment.
 CC -!- TISSUE SPECIFICITY: Widely expressed. High levels in kidney,
 CC prostate, testis and ovary.
 CC -!- DISEASE: Defects in ZMPSTE24 are the cause of mandibuloacral
 CC dysplasia with type B lipodystrophy (MADB) [MIM:608612].
 CC Mandibuloacral dysplasia (MAD) is a rare autosomal recessive
 CC disorder characterized by mandibular and clavicular hypoplasia,
 CC acroosteolysis, delayed closure of the cranial suture, joint
 CC contractures, and types A or B patterns of lipodystrophy. Type B
 CC lipodystrophy observed in MADB, is characterized by generalized
 CC fat loss.
 CC -!- SIMILARITY: Belongs to the peptidase M48A family.
 CC -----
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 CC -----
 DR EMBL; AB016068; BAA33727.1; -; mRNA.
 DR EMBL; AF064867; AAC68866.1; -; mRNA.
 DR EMBL; Y13834; CAB46277.1; -; mRNA.
 DR EMBL; AL050341; CAB81610.1; -; Genomic_DNA.
 DR EMBL; BC037283; AAH37283.1; -; mRNA.
 DR MEROPS; M48.003; -.

DR Ensembl; ENSG00000084073; Homo sapiens.
 DR HGNC; HGNC:12877; ZMPSTE24.
 DR MIM; 606480; gene.
 DR MIM; 608612; phenotype.
 DR GO; GO:0008235; F:metalloexopeptidase activity; TAS.
 DR GO; GO:0006508; P:proteolysis and peptidolysis; TAS.
 DR InterPro; IPR006025; Pept_M_Zn_BS.
 DR InterPro; IPR001915; Peptidase_M48.
 DR Pfam; PF01435; Peptidase_M48; 1.
 DR PROSITE; PS00142; ZINC_PROTEASE; FALSE_NEG.
 KW Disease mutation; Endoplasmic reticulum; Golgi stack; Hydrolase;
 KW Membrane; Metal-binding; Metalloprotease; Protease; Transmembrane;
 KW Zinc.
 FT CHAIN 1 475 CAAX prenyl protease 1 homolog.
 FT /FTId=PRO_0000138844.
 FT TRANSMEM 19 39 Potential.
 FT TRANSMEM 82 102 Potential.
 FT TRANSMEM 124 144 Potential.
 FT TRANSMEM 171 191 Potential.
 FT TRANSMEM 196 216 Potential.
 FT TRANSMEM 348 368 Potential.
 FT TRANSMEM 383 405 Potential.
 FT ACT_SITE 336 336 By similarity.
 FT ACT_SITE 419 419 Proton donor (By similarity).
 FT METAL 335 335 Zinc (catalytic) (By similarity).
 FT METAL 339 339 Zinc (catalytic) (By similarity).
 FT METAL 415 415 Zinc (catalytic) (By similarity).
 FT VARIANT 340 340 W -> R (in MADB).
 FT /FTId=VAR_019308.
 FT CONFLICT 16 16 E -> K (in Ref. 1).
 FT CONFLICT 137 137 T -> A (in Ref. 5; AAH37283).
 SQ SEQUENCE 475 AA; 54813 MW; 6C49179DEB0C8F7F CRC64;

Alignment Scores:

Pred. No.:	9.88e-64	Length:	475
Score:	567.00	Matches:	115
Percent Similarity:	95.8%	Conservative:	0
Best Local Similarity:	95.8%	Mismatches:	5
Query Match:	87.9%	Indels:	1
DB:	1	Gaps:	0

US-10-646-950-6 (1-362) x FACE1_HUMAN (1-475)

Qy	2	ATTATTAGCCAGATGAATTCCTTTCTGTGTTTTTTTTTTATTTGCTGTATTAATTGGTCTGA	61
Db	350	IleIleSerGlnMetAsnSerPheLeuCysPhePheLeuPheAlaValLeuIleGlyArg	369
Qy	62	AAGGAGCTTTTGTGTCATTTGGTTTTTATGNTAGCCAACCCACTNTTATTGGACTATTG	121
Db	370	LysGluLeuPheAlaAlaPheGlyPheTyrAspSerGlnProThrLeuIleGlyLeuLeu	389
Qy	122	NTCATCTTCCAGTTTATTTTTTACCTTACAATGNGGTTCTTTCTTTTGCCTAACAGTC	181
Db	390	IleIlePheGlnPheIlePheSerProTyrAsnGluValLeuSerPheCysLeuThrVal	409
Qy	182	CTAAGCCGAGATTGAGTTTCAAGCTGATGCATT-GCCAAGAACTTGGGAAGGCTAAA	240
Db	410	LeuSerArgArgPheGluPheGlnAlaAspAlaPheAlaLysLysLeuGlyLysAlaLys	429
Qy	241	GACTTATATTCTGCTTTAATCAAACCTTAACAAAGATAACTTGGGATTCCTGTTTCTGAC	300
Db	430	AspLeuTyrSerAlaLeuIleLysLeuAsnLysAspAsnLeuGlyPheProValSerAsp	449
Qy	301	TGGTTGTTCTCAATGTGGCATTATTCTCATCCTCCACTGCTAGAGAGACTTCAAGCTTTG	360
Db	450	TrpLeuPheSerMetTrpHisTyrSerHisProProLeuLeuGluArgLeuGlnAlaLeu	469